



SEQUENCE LISTING

<110> Sanders, Bob G.
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Yu, Weiping
Liu, Hui
Hantash, Feras

<120> Tocopherol Associated Protein and Uses Thereof

<130> D6453CIP

<140> US 10/696,699
<141> 2003-10-29

<150> US 10/419,629
<151> 2003-04-21

<160> 19

<210> 1
<211> 1137
<212> DNA
<213> *Homo sapiens*

<220>
<223> TAP-38 gene sequence

<400> 1

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tgtggagttc	cgaaagcaaa	aggacattga	caacatcatt	agcatggcag	150
cctccagagg	tgatccaaca	gtatctgtca	ctggatgcc	agggtctgct	200
gttctcagcc	tccaaacagg	acctgctgag	gaccaagatg	ctggatgcc	250
agggtctgct	gttctcagcc	tccaaacagg	acctgctgag	gaccaagatg	300
cgggagtgtg	agctgcttct	gcaagagtgt	gcccaccaga	ccacaaagtt	350
ggggaggaag	gtggagacca	tcaccataat	ttatgactgc	gaggggcttg	400
gcctcaagca	tctcttgaag	cctgctgtgg	aggcctatgg	agagttctc	450
tgcatgtttg	agaaaaat	tcccgaaaca	ctgaagcg	tttttgtt	500
taaagcccccc	aaactgtttc	ctgtggccta	taacctcatc	aaacccttcc	550
tgagtgagga	cactcgtaag	aagatcatgg	tcctgggagc	aaatttggaa	600
gaggttttac	tgaaacat	cagccctgac	caggtgcctg	tggagttatgg	650
gggcgcctatg	actgaccctg	atgaaaaccc	caagtgc	tccaagatca	700
actacgggggg	tgacatcccc	aggaagtatt	atgtgcgaga	ccaggtgaaa	750
cagcagtatg	aacacagcgt	gcagattcc	cgtggctcct	cccaccaagt	800
ggagttatgag	atccctttcc	ctgctgtgt	cctcagggtgg	cagtttatgt	850
cagatggagc	ggatgttgg	tttgggattt	tcctgaagac	caagatggga	900
gagaggcagc	gggcagggg	gatgacagag	gtgctgccc	accagaggta	950
caactcccac	ctggccctg	aagatggac	cctcacctgc	agtgatcctg	1000
gcatctatgt	cctgcgg	gacaacacct	acagttcat	tcatgccaag	1050
aaggtaatt	tcactgtgga	ggtcctgctt	ccagacaaag	cctcagaaga	1100

gaagatgaaa cagctggggg caggcacccc gaaataa

1137

<210> 2
<211> 378
<212> PRT
<213> *Homo sapiens*

<220>
<221> PEPTIDE
<223> TAP-38 polypeptide

<400> 2
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5 10 15
Leu Ala Lys Pro Glu Ala Ser Thr Cys Arg Ser Arg Arg Pro Cys
20 25 30
Ser Gly Ser Met Trp Ser Ser Glu Ser Lys Arg Thr Leu Thr Thr
35 40 45
Ser Leu Ala Trp Gln Pro Pro Glu Val Ile Gln Gln Tyr Leu Ser
50 55 60
Gly Gly Met Cys Gly Tyr Asp Leu Asp Gly Cys Pro Val Trp Tyr
65 70 75
Asp Ile Ile Gly Pro Lys Asp Ala Lys Gly Leu Leu Phe Ser Ala
80 85 90
Ser Lys Gln Asp Leu Leu Arg Thr Lys Met Arg Glu Cys Glu Leu
95 100 105
Leu Leu Gln Glu Cys Ala His Gln Thr Thr Lys Leu Gly Arg Lys
110 115 120
Val Glu Thr Ile Thr Ile Ile Tyr Asp Cys Glu Gly Leu Gly Leu
125 130 135
Lys His Leu Trp Lys Pro Ala Val Glu Ala Tyr Gly Glu Phe Leu
140 145 150
Cys Met Phe Glu Glu Asn Tyr Pro Glu Thr Leu Lys Arg Leu Phe
155 160 165
Val Val Lys Ala Pro Lys Leu Phe Pro Val Ala Tyr Asn Leu Ile
170 175 180
Lys Pro Phe Leu Ser Glu Asp Thr Arg Lys Lys Ile Met Val Leu
185 190 195
Gly Ala Asn Tyr Lys Glu Val Leu Leu Lys His Ile Ser Pro Asp
200 205 210
Gln Val Pro Val Glu Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly
215 220 225
Asn Pro Lys Cys Lys Ser Lys Ile Asn Tyr Gly Gly Asp Ile Pro
230 235 240
Arg Lys Tyr Tyr Val Arg Asp Gln Val Lys Gln Gln Tyr Glu His
245 250 255
Ser Val Gln Ile Ser Arg Gly Ser Ser His Gln Val Glu Tyr Glu
260 265 270
Ile Leu Phe Pro Gly Cys Val Leu Arg Trp Gln Phe Met Ser Asp
275 280 285

SEQ 2

Gly Ala Asp Val Gly Phe Gly Ile Phe Leu Lys Thr Lys Met Gly
 290 295 300
 Glu Arg Gln Arg Ala Gly Glu Met Thr Glu Val Leu Pro Asn Gln
 305 310 315
 Arg Tyr Asn Ser His Leu Val Pro Glu Asp Gly Thr Leu Thr Cys
 320 325 330
 Ser Asp Pro Gly Ile Tyr Val Leu Arg Phe Asp Asn Thr Tyr Ser
 335 340 345
 Phe Ile His Ala Lys Lys Val Asn Phe Thr Val Glu Val Leu Leu
 350 355 360
 Pro Asp Lys Ala Ser Glu Glu Lys Met Lys Gln Leu Gly Ala Gly
 365 370 375
 Thr Pro Lys

<210> 3
 <211> 1212
 <212> DNA
 <213> *Homo sapiens*

<220>
 <223> TAP-46 gene sequence

<400> 3

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atgactattt	tctcctgcgt	tggctccgag	ccagaagctt	cgacctgcag	150
aagtccggagg	ccatgctccg	gaagcatgtg	gagttccgaa	agcaaaaagga	200
cattgacaac	atcatttagct	ggcagcctcc	agaggtgatc	caacagtatc	250
tgtcaactgga	tgccaagggt	ctgctgttct	cagcctccaa	acaggacactg	300
ctgaggacca	agatgctgga	tgccaagggt	ctgctgttct	cagcctccaa	350
acaggacactg	ctgaggacca	agatgcggga	gtgtgagctg	cttctgcaag	400
agtgtgccca	ccagaccaca	aagttgggga	ggaaggtgga	gaccatcacc	450
ataatttatg	actgcgaggg	gctggcctc	aagcatctct	ggaaggctgc	500
tgtggaggcc	tatggagagt	ttctctgcat	gtttgagaa	aattatcccg	550
aaacactgaa	gcgtctttt	gttgttaaaag	cccccaaact	gttcctgtg	600
gcctataacc	tcatcaaacc	cttccctgagt	gaggacactc	gtaagaagat	650
catggtcctg	ggagcaaatt	ggaaggaggt	tttactgaaa	catatcagcc	700
ctgaccaggt	gctctggag	tatggggcgc	ccatgactga	ccctgatgga	750
aaccccaagt	gcaaatccaa	gatcaactac	gggggtgaca	tccccaggaa	800
gtatttatgt	cgagaccagg	tgaaacagca	gtatgaacac	agcgtgcaga	850
tttcccgtgg	ctcctcccac	caagtggagt	atgagatcct	cttccctggc	900
tgtgtcctca	ggtggcagtt	tatgtcagat	ggagcggatg	ttggtttgg	950
gattttcctg	aagaccaaga	tgggagagag	gcagcggca	ggggagatga	1000
cagaggtgct	gcccaaccag	aggtacaact	cccacctgg	ccctgaagat	1050
gggaccctca	cctgcagtga	tcctggcatc	tatgtcctgc	gtttgacaa	1100
cacctacagc	ttcattcatg	ccaagaaggt	caatttcaact	gtggaggtcc	1150
tgcttccaga	caaagcctca	gaagagaaga	tgaaacagct	ggggcaggc	1200
accccgaaat	aa				1212

<210> 4
<211> 403
<212> PRT
<213> *Homo sapiens*

<220>
<221> PEPTIDE
<223> TAP-46 polypeptide

<400> 4
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Leu Ala Lys Phe Arg Glu Asn Val Gln Asp Val Leu Pro Ala Leu
20 25 30
Pro Asn Pro Asp Asp Tyr Phe Leu Leu Arg Trp Leu Arg Ala Arg
35 40 45
Ser Phe Asp Leu Gln Lys Ser Glu Ala Met Leu Arg Lys His Val
50 55 60
Glu Phe Arg Lys Gln Lys Asp Ile Asp Asn Ile Ile Ser Trp Gln
65 70 75
Pro Pro Glu Val Ile Gln Gln Tyr Leu Ser Gly Gly Met Cys Gly
80 85 90
Tyr Asp Leu Asp Gly Cys Pro Val Trp Tyr Asp Ile Ile Gly Pro
95 100 105
Leu Asp Ala Lys Gly Leu Leu Phe Ser Ala Ser Lys Gln Asp Leu
110 115 120
Leu Arg Thr Lys Met Arg Glu Cys Glu Leu Leu Leu Gln Glu Cys
125 130 135
Ala His Gln Thr Thr Lys Leu Gly Arg Lys Val Glu Thr Ile Thr
140 145 150
Ile Ile Tyr Asp Cys Glu Gly Leu Gly Leu Lys His Leu Trp Lys
155 160 165
Pro Ala Val Glu Ala Tyr Gly Glu Phe Leu Cys Met Phe Glu Glu
170 175 180
Asn Tyr Pro Glu Thr Leu Lys Arg Leu Phe Val Val Lys Ala Pro
185 190 195
Lys Leu Phe Pro Val Ala Tyr Asn Leu Ile Lys Pro Phe Leu Ser
200 205 210
Glu Asp Thr Arg Lys Lys Ile Met Val Leu Gly Ala Asn Trp Lys
215 220 225
Glu Val Leu Leu Lys His Ile Ser Pro Asp Gln Val Pro Val Glu
230 235 240
Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Lys
245 250 255
Ser Lys Ile Asn Tyr Gly Gly Asp Ile Pro Arg Lys Tyr Tyr Val
260 265 270
Arg Asp Gln Val Lys Gln Gln Tyr Glu His Ser Val Gln Ile Ser
275 280 285
Arg Gly Ser Ser His Gln Val Glu Tyr Glu Ile Leu Phe Pro Gly
290 295 300
Cys Val Leu Arg Trp Gln Phe Met Ser Asp Gly Ala Asp Val Gly
305 310 315

Phe Gly Ile Phe Leu Lys Thr Lys Met Gly Glu Arg Gln Arg Ala
320 325 330
Gly Glu Met Thr Glu Val Leu Pro Asn Gln Arg Tyr Asn Ser His
335 340 345
Leu Val Pro Glu Asp Gly Thr Leu Thr Cys Ser Asp Pro Gly Ile
350 355 360
Tyr Val Leu Arg Phe Asp Asn Thr Tyr Ser Phe Ile His Ala Lys
365 370 375
Lys Val Asn Phe Thr Val Glu Val Leu Leu Pro Asp Lys Ala Ser
380 385 390
Glu Glu Lys Met Lys Gln Leu Gly Ala Gly Thr Pro Lys
395 400

<210> 5
<211> 21
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> TAP-38 sense oligonucleotide

<400> 5
atgagcggca gagtcggcgta t 21

<210> 6
<211> 23
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> TAP-38 antisense oligonucleotide

<400> 6
ttatccgggtgcctgccc cca 23

<210> 7
<211> 57
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> TAP-38 sense oligonucleotide encoding HA-tag

<400> 7
cgcgaaattca tgtatgatgt tcctgattat gctagcctca gccccagagt 50
cggcgat 57

<210> 8
<211> 16
<212> PRT
<213> *Homo sapiens*
<220>
<221> PEPTIDE
<223> 16 amino acids from the c-terminus of TAP attached
to keyhole limpet hemocyanin

<400> 8
Lys Ala Ser Glu Glu Lys Met Lys Gln Leu Gly Ala Gly Thr Pro
5 10 15
Lys

<210> 9
<211> 27
<212> DNA
<213> artificial sequence

<220>
<221> CDS
<223> sequence for an HA tag

<400> 9
tatgatgttc ctgattatgc tagcctc 27

<210> 10
<211> 59
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> sense primer for the deletion mutant TAP-882

<400> 10
cgcgaattca tgtatgtat tcctgattat gctagcctcc tgctgttctc 50
agcctccaa 59

<210> 11
<211> 59
<212> DNA
<213> artificial sequence

<220>
<221> primer_bind
<223> sense primer for the deletion mutant TAP-681

<400> 11					
cgcgaattca	tgtatgatgt	tcctgattat	gctagcctct	ttgaggaaaa	50
ttatcccgaa					59
<210> 12					
<211>	59				
<212>	DNA				
<213>	artificial sequence				
<220>					
<221>	primer_bind				
<223>	sense primer for the deletion mutant TAP-456				
<400> 12					
cgcgaattca	tgtatgatgt	tcctgattat	gctagcctca	agtgcaaatc	50
caagatcaa					59
<210> 13					
<211>	21				
<212>	DNA				
<213>	artificial sequence				
<220>					
<221>	primer_bind				
<223>	antisense primer for the TAP deletion mutants				
<400> 13					
tttcgggttg	cctgccccca	g	21		
<210> 14					
<211>	882				
<212>	DNA				
<213>	<i>Homo sapiens</i>				
<220>					
<223>	deletion mutant TAP-882				
<400> 14					
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gtgtgagctg	cttctgcaag	agtgtgccca	ccagaccaca	aagttgggga	100
ggaagggtgga	gaccatcacc	ataatttatg	actgcgaggg	gcttggcctc	150
aagcatctct	ggaagcctgc	tgtggaggcc	tatggagagt	ttctctgcat	200
gtttgaggaa	aattatcccg	aaacactgaa	gcgtctttt	gttgttaaag	250
cccccaaact	gttcctgtg	gcctataacc	tcatcaaacc	cttcctgagt	300
gaggacactc	gtaagaagat	catggcctg	ggagcaaatt	ggaaggaggt	350
tttactgaaa	catatcagcc	ctgaccaggt	gcctgtggag	tatggggca	400
ccatgactga	ccctgatgga	aaccccaagt	gcaaatcaa	gatcaactac	450
gggggtgaca	tccccagggaa	gtattatgtg	cgagaccagg	tgaaacagca	500
gtatgaacac	agcgtgcaga	tttcccgtgg	ctcctccac	caagtggagt	550

atgagatcet cttccctggc tgcgtcctca ggtggcagtt tatgtcagat 600
ggagcggatg ttggtttgg gatttcctg aagaccaaga tgggagagag 650
gcagcggca ggggagatga cagaggtgct gcccaaccag aggtacaact 700
cccacctggc cccctgaagat gggaccctca cctgcagtga tcctgcac 750
tatgtcctgc ggttgacaa cacctacagc ttcattcatg ccaagaagg 800
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tgaaacagct gggggcaggc accccgaaat aa 882

<210> 15
<211> 293
<212> PRT
<213> *Homo sapiens*

<220>
<221> PEPTIDE
<223> deletion mutant TAP-882

<400> 15
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Arg Glu Cys Glu Leu Leu Leu Gln Glu Cys Ala His Gln Thr Thr
20 25 30
Lys Leu Gly Arg Lys Val Glu Thr Ile Thr Ile Ile Tyr Asp Cys
35 40 45
Glu Gly Leu Gly Leu Lys His Leu Trp Lys Pro Ala Val Glu Ala
50 55 60
Tyr Gly Glu Phe Leu Cys Met Phe Glu Glu Asn Tyr Pro Glu Thr
65 70 75
Leu Lys Arg Leu Phe Val Val Lys Ala Pro Lys Leu Phe Pro Val
80 85 90
Ala Tyr Asn Leu Ile Lys Pro Phe Leu Ser Glu Asp Thr Arg Lys
95 100 105
Lys Ile Met Val Leu Gly Ala Asn Trp Lys Glu Val Leu Leu Lys
110 115 120
His Ile Ser Pro Asp Gln Val Pro Val Glu Tyr Gly Gly Thr Met
125 130 135
Thr Asp Pro Asp Gly Asn Pro Lys Cys Lys Ser Lys Ile Asn Tyr
140 145 150
Gly Gly Asp Ile Pro Arg Lys Tyr Tyr Val Arg Asp Gln Val Lys
155 160 165
Gln Gln Tyr Glu His Ser Val Gln Ile Ser Arg Gly Ser Ser His
170 175 180
Gln Val Glu Tyr Glu Ile Leu Phe Pro Gly Cys Val Leu Arg Trp
185 190 195
Gln Phe Met Ser Asp Gly Ala Asp Val Gly Phe Gly Ile Phe Leu
200 205 210
Lys Thr Lys Met Gly Glu Arg Gln Arg Ala Gly Glu Met Thr Glu
215 220 225
Val Leu Pro Asn Gln Arg Tyr Asn Ser His Leu Val Pro Glu Asp
230 235 240

Gly	Thr	Leu	Thr	Cys	Ser	Asp	Pro	Gly	Ile	Tyr	Val	Leu	Arg	Phe
				245						250				255
Asp	Asn	Thr	Tyr	Ser	Phe	Ile	His	Ala	Lys	Lys	Val	Asn	Phe	Thr
				260					265				270	
Val	Glu	Val	Leu	Leu	Pro	Asp	Lys	Ala	Ser	Glu	Glu	Lys	Met	Lys
				275					280				285	
Gln	Leu	Gly	Ala	Gly	Thr	Pro	Lys							
				290										

<210> 16
 <211> 681
 <212> DNA
 <213> *Homo sapiens*

<220>
 <223> deletion mutant TAP-681

<400> 16
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 ccccaaactg ttccctgtgg cctataacct catcaaacc ttcctgagtg 100
 aggacactcg taagaagatc atggtcctgg gagcaaattg gaaggagggt 150
 ttactgaaac atatcagccc tgaccaggtg cctgtggagt atgggggcac 200
 catgactgac cctgatggaa accccaagtg caaatccaag atcaactacg 250
 ggggtgacat ccccaggaag tattatgtgc gagaccaggt gaaacagcag 300
 tatgaacaca gcgtgcagat ttcccgtggc tcctccacc aagtggagta 350
 tgagatcctc ttccctggct gtgcctcag gtggcagttt atgtcagatg 400
 gagcggatgt tggtttggg atttcctga agaccaagat gggagagagg 450
 cagcggggcag gggagatgac agaggtgctg cccaaccaga ggtacaactc 500
 ccacctggtc cctgaagatg ggaccctcac ctgcagtgtat cctggcatct 550
 atgtcctgctg gtttgacaac acctacagct tcattcatgc caagaaggtc 600
 aatttcactg tggaggtcct gcttccagac aaaccctcag aagagaagat 650
 gaaacagctg gggcaggca ccccgaaata a 681

<210> 17
 <211> 226
 <212> PRT
 <213> *Homo sapiens*

<220>
 <221> PEPTIDE
 <223> deletion mutant TAP-681

<400> 17
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 5 10 15
 Lys Ala Pro Lys Leu Phe Pro Val Ala Tyr Asn Leu Ile Lys Pro
 20 25 30
 Phe Leu Ser Glu Asp Thr Arg Lys Lys Ile Met Val Leu Gly Ala
 35 40 45

Asn Trp Lys Glu Val Leu Leu Lys His Ile Ser Pro Asp Gln Val
 50 55 60
 Pro Val Glu Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly Asn Pro
 65 70 75
 Lys Cys Lys Ser Lys Ile Asn Tyr Gly Gly Asp Ile Pro Arg Lys
 80 85 90
 Tyr Tyr Val Arg Asp Gln Val Lys Gln Gln Tyr Glu His Ser Val
 95 100 105
 Gln Ile Ser Arg Gly Ser Ser His Gln Val Glu Tyr Glu Ile Leu
 110 115 120
 Phe Pro Gly Cys Val Leu Arg Trp Gln Phe Met Ser Asp Gly Ala
 125 130 135
 Asp Val Gly Phe Gly Ile Phe Leu Lys Thr Lys Met Gly Glu Arg
 140 145 150
 Gln Arg Ala Gly Glu Met Thr Glu Val Leu Pro Asn Gln Arg Tyr
 155 160 165
 Asn Ser His Leu Val Pro Glu Asp Gly Thr Leu Thr Cys Ser Asp
 170 175 180
 Pro Gly Ile Tyr Val Leu Arg Phe Asp Asn Thr Tyr Ser Phe Ile
 185 190 195
 His Ala Lys Lys Val Asn Phe Thr Val Glu Val Leu Leu Pro Asp
 200 205 210
 Lys Ala Ser Glu Glu Lys Met Lys Gln Leu Gly Ala Gly Thr Pro
 215 220 225
 Lys

<210> 18
 <211> 456
 <212> DNA
 <213> *Homo sapiens*

<220>
 <223> deletion mutant TAP-456

<400> 18
 aagtgccaa at ccaagatcaa ctacgggggt gacatccccca ggaaggatttta 50
 ttgtcgagac caggtgaaac agcagtatga acacagcggtg cagatttccc 100
 gtggctcc tc ccaccaagtg gagttatgaga tccttccccc tggctgtgtc 150
 ctcagggtggc agtttatgtc agatggagcg gatgttggtt ttgggatttt 200
 cctgaagacc aagatgggag agaggcagcg ggcaggggag atgacagagg 250
 tgctgcccaa ccagaggtac aactccacc tggcccttga agatgggacc 300
 ctcacctgca gtgatcctgg catctatgtc ctgcggttt acaacaccta 350
 cagcttcatt catgccaaga aggtcaattt cactgtggag gtcctgcttc 400
 cagacaaagc ctcagaagag aagatgaaac agctgggggc aggcaccccg 450
 aaataa 456

<210> 19
 <211> 151
 <212> PRT
 <213> *Homo sapiens*

<220>

<221> PEPTIDE

<223> deletion mutant TAP-456

<400> 19

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				5				10						15
Tyr	Tyr	Val	Arg	Asp	Gln	Val	Lys	Gln	Gln	Tyr	Glu	His	Ser	Val
				20				25						30
Gln	Ile	Ser	Arg	Gly	Ser	Ser	His	Gln	Val	Glu	Tyr	Glu	Ile	Leu
				35				40						45
Phe	Pro	Gly	Cys	Val	Leu	Arg	Trp	Gln	Phe	Met	Ser	Asp	Gly	Ala
				50				55						60
Asp	Val	Gly	Phe	Gly	Ile	Phe	Leu	Lys	Thr	Lys	Met	Gly	Glu	Arg
				65				70						75
Gln	Arg	Ala	Gly	Glu	Met	Thr	Glu	Val	Leu	Pro	Asn	Gln	Arg	Tyr
				80				85						90
Asn	Ser	His	Leu	Val	Pro	Glu	Asp	Gly	Thr	Leu	Thr	Cys	Ser	Asp
				95				100						105
Pro	Gly	Ile	Tyr	Val	Leu	Arg	Phe	Asp	Asn	Thr	Tyr	Ser	Phe	Ile
				110				115						120
His	Ala	Lys	Lys	Val	Asn	Phe	Thr	Val	Glu	Val	Leu	Leu	Pro	Asp
				125				130						135
Lys	Ala	Ser	Glu	Glu	Lys	Met	Lys	Gln	Leu	Gly	Ala	Gly	Thr	Pro
				140				145						150
Lys														